

SEQUENCE LISTING

<110> Degussa-Hüls AG
Forschungszentrum Jülich GmbH

<120> L-Lysine-producing corynebacteria and
process for the preparation of lysine.

<130> 980183 BT

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<160> 6

<170> PatentIn Ver. 2.1

<210> 1

<211> 795

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> -35_signal

<222> (774)..(779)

<220>

<223> DNA upstream from dapB

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<222> (851)..(1594)

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tccggtatcg atacctggaa cgacaacctg atcaggatat ccagtgcctt gaattattgac 180

10 gttgaggaag gaatcaccag ccattctcaac tggaagacct gacgcctgct gaattggatc 240

agtggcccaa tcgaccacc aaccagggtg gccattaccg gcgatatcaa aaacaactcg 300

tgtgaacggt tcgtgctcgg caacgcggat gccagcgatc gacatatcgg agtcaccaac 360

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25 taagtctcat atttcaaaca tagttccacc tgtgtgatta atccctagaa cggaacaaac 720

tgatgaacaa tcgttaacaa cacagaccaa aacggtcagt taggtatgga tatcagcacc 780

30 ttctgaacgg gtacgtctag actggtgggc gtttgaaaaa ctcttcgccc caggaatg 840

aaggagcata atg gga atc aag gtt ggc gtt ctg gga gcc aaa ggc cgt 889

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35 gtt ggt caa act att gtg gca gca gtc aat gag tcc gac gat ctg gag 937

Val Gly Gln Thr Ile Val Ala Ala Val Asn Glu Ser Asp Asp Leu Glu

15 20 25

40 ctt gtt gca gag atc ggc gtc gac gat gat ttg agc ctt ctg gta gac 985

Leu Val Ala Glu Ile Gly Val Asp Asp Asp Leu Ser Leu Leu Val Asp

30 35 40 45

45 aac ggc gct gaa gtt gtc gtt gac ttc acc act cct aac gct gtg atg 1033

Asn Gly Ala Glu Val Val Val Asp Phe Thr Thr Pro Asn Ala Val Met

50 55 60

ggc aac ctg gag ttc tgc atc aac aac ggc att tct gcg gtt gtt gga 1081

Gly Asn Leu Glu Phe Cys Ile Asn Asn Gly Ile Ser Ala Val Val Gly

65 70 75

50 acc acg ggc ttc gat gat gct cgt ttg gag cag gtt cgc gac tgg ctt 1129

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80 85 90

55 gaa gga aaa gac aat gtc ggt gtt ctg atc gca cct aac ttt gct atc 1177

Glu Gly Lys Asp Asn Val Gly Val Leu Ile Ala Pro Asn Phe Ala Ile

95 100 105

60 tct gcg gtg ttg acc atg gtc ttt tcc aag cag gct gcc cgc ttc ttc 1225

Ser Ala Val Leu Thr Met Val Phe Ser Lys Gln Ala Ala Arg Phe Phe

110 115 120 125

gaa tca gct gaa gtt att gag ctg cac cac ccc aac aag ctg gat gca 1273
 Glu Ser Ala Glu Val Ile Glu Leu His His Pro Asn Lys Leu Asp Ala
 130 135 140

5 cct tca ggc acc gcg atc cac act gct cag ggc att gct gcg gca cgc 1321
 Pro Ser Gly Thr Ala Ile His Thr Ala Gln Gly Ile Ala Ala Ala Arg
 145 150 155

10 aaa gaa gca ggc atg gac gca cag cca gat gcg acc gag cag gca ctt 1369
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 160 165 170

15 gag ggt tcc cgt ggc gca agc gta gat gga atc ccg gtt cat gca gtc 1417
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20 cgc atg tcc ggc atg gtt gct cac gag caa gtt atc ttt ggc acc cag 1465
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 190 195 200 205

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 Gly Gln Thr Leu Thr Ile Lys Gln Asp Ser Tyr Asp Arg Asn Ser Phe
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25 gca cca ggt gtc ttg gtg ggt gtg cgc aac att gca cag cac cca ggc 1561
 Ala Pro Gly Val Leu Val Gly Val Arg Asn Ile Ala Gln His Pro Gly
 225 230 235

30 cta gtc gta gga ctt gag cat tac cta ggc ctg taaaggctca tttcagcagc 1614
 Leu Val Val Gly Leu Glu His Tyr Leu Gly Leu
 240 245

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35 ggagttgata gcgtgcagtt cttttactcc acccgctgat gttgagtggc caactgatgt 1734

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45 <213> Corynebacterium glutamicum

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 35 40 45

Glu Val Val Val Asp Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu
 50 55 60

60 Glu Phe Cys Ile Asn Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly
 65 70 75 80

Phe Asp Asp Ala Arg Leu Glu Gln Val Arg Asp Trp Leu Glu Gly Lys
 85 90 95
 5 Asp Asn Val Gly Val Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val
 100 105 110
 Leu Thr Met Val Phe Ser Lys Gln Ala Ala Arg Phe Phe Glu Ser Ala
 115 120 125
 10 Glu Val Ile Glu Leu His His Pro Asn Lys Leu Asp Ala Pro Ser Gly
 130 135 140
 Thr Ala Ile His Thr Ala Gln Gly Ile Ala Ala Ala Arg Lys Glu Ala
 145 150 155 160
 15 Gly Met Asp Ala Gln Pro Asp Ala Thr Glu Gln Ala Leu Glu Gly Ser
 165 170 175
 20 Arg Gly Ala Ser Val Asp Gly Ile Pro Val His Ala Val Arg Met Ser
 180 185 190
 Gly Met Val Ala His Glu Gln Val Ile Phe Gly Thr Gln Gly Gln Thr
 195 200 205
 25 Leu Thr Ile Lys Gln Asp Ser Tyr Asp Arg Asn Ser Phe Ala Pro Gly
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 225 230 235 240
 30 Gly Leu Glu His Tyr Leu Gly Leu
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 50 <210> 5
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 55 <223> Description of the synthetic sequence:
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 60 <220>
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- 5 <210> 6
- <211> 80
- <212> DNA
- <213> Synthetic sequence

- 10 <220>
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- 15 <220>
- <221> mutation
- <222> (35)..(53)

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ctatgagcac aggtttaaca 80